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## Comments on the identities of two subspecies from Uighur Ili (*Lepidoptera*, *Arctiidae*)

Sibel Kızıldağ<sup>1</sup> Muhabbet Kemal Ahmet Ömer Koçak

**Abstract:** Comments on the identities of two subspecies from Uighur Ili (*Lepidoptera*, *Arctiidae*). *Misc. Pap.* 179: 1-4, 4 figs.

This paper deals with the comments on their first mtCOI sequences of two subspecies, *Arctia caja roshengul* and *Phragmatobia fuliginosa paghmani* (*Arctiidae*) from Uighur Ili. Their identities at the subspecies level are discussed from the molecular standpoint.

**Key words:** *Arctia*, *caja*, *roshengul*, *Phragmatobia*, *fuliginosa*, *paghmani*, *Arctiidae*, *Lepidoptera*, Uighur Ili, Afghanistan, Europe, Asia, MtCOI sequence, comment, taxonomy.

In the recent publication, the authors reported two arctiid species from Uighur Ili: *Arctia caja* ssp. *roshengul*, and *Phragmatobia fuliginosa* ssp. *paghmani* (Kemal & Koçak, 2018). The present study was aimed at establishing the mitochondrial COI sequences of the subspecies of *Arctia caja* and *Phragmatobia fuliginosa* from Uighur Ili and other regions for identification, and more importantly, to evaluate subspecies differentiation. The MtCOI sequences of our species are prepared successfully, and the results obtained compared with those of some populations of the “published & released data” given currently in the Bold Systems (Ratnasingham & Hebert, 2007). About the subspecific identities of these taxa, our comments are given below.

The material used here are in the Collection of the Cesa. Privately obtained MtCOI sequences are preserved in the Gen Bank of the Cesa<sup>2</sup>. Our surveys on these subjects are still ongoing.

### *Arctia caja* subsp. *roshengul* Kemal & Koçak

(Figs. 1,3)

*Arctia caja* subsp. *roshengul* Kemal & Koçak, 2018, *Priamus* 17 (3): 211. Holotype ♀. Uighur Ili, Ili Region, Tekes, Kichikkuşay.

Range: Uighur Ili.

Comments: A new subspecies of *Arctia* (s.str.) *caja* ssp. *roshengul* (*Arctiidae*) was firstly described by Kemal and Koçak (2018) from Uighur Ili. Described subspecies is allopatric,

<sup>1</sup> Dr. Sibel Kızıldağ & Dr. Muhabbet Kemal - Van Yüzüncü Yıl University, Faculty of Science, Dept. of Biology, Campus, Van / Turkey.

e-mails: [sibelkizildag@yyu.edu.tr](mailto:sibelkizildag@yyu.edu.tr) - [muhabbet\\_kemal@yahoo.com.tr](mailto:muhabbet_kemal@yahoo.com.tr)

Prof. em. Dr. Ahmet Ömer Koçak, c/o Yüzüncü Yıl University, Faculty of Science, Dept. of Biology., Van / Turkey.

e-mail: [cesa\\_tr@yahoo.com.tr](mailto:cesa_tr@yahoo.com.tr)

<sup>2</sup> GenBank of the Cesa is a private attempt and its webpage under construction. Limited information are currently accessible at the following address: <http://entcesa.tripod.com/Cesacollection.pdf>

phenotypically distinct (in colouration and wing pattern), and has at least one fixed diagnosable character state. On the other hand, the populations of *Arctia caja*, inhabiting in “Xinjiang” [Uighur Ili] were attributed by Dubatolov (2010) to the nominate *caja*, without giving collecting locality and comment. This region is very large area (642,820 sq mi); therefore this attribution was met with suspicion. Thereupon, the MtCOI sequence was prepared and compared with the European populations of *caja*, and also with other neighbour populations. In recent years, MtCOI sequences of *Arctia caja* were obtained in different geographic regions. However, there is no evaluation to the molecular level in the subspecies. In this study, the mtCOI gene sequence of this subspecies was firstly obtained (658 bp) and the phylogenetic tree supported it as a distinct subspecies. The estimated evolutionary divergence (using the Kimura 2-parameter model) between American and European *Arctia caja* was 0-0.022, while between populations of Russia (Ussuri) and Europa was 0.025-0.036. There was greater genetic divergence between phenotypically indistinguishable specimens of *Arctia caja* of Russia (Altay) in phylogenetic tree. *Arctia caja* ssp. *roshengul* was determined closer to the European than to the Russian populations.

According to this result, five different subspecies of this species can be offered, and in the present study, *Arctia caja roshengul* has been proved as a distinct subspecies. This case is clearly supported by the molecular characters.

The low bootstrap values in the tree topology indicate that more molecular data are needed for subspecies of this species from different geographies. Moreover, we have only evaluated the different populations of this species in different regions, since there is no subspecies barcoding in the GenBank and BOLDsystem.

### ***Phragmatobia fuliginosa* subsp. *paghmani* Lének (Figs. 2,4)**

*Phragmatobia fuliginosa* subsp. *paghmani* Lének, 1966, *Z. Wien. ent. Ges.* 51: 105-106. Holotype ♂: Afghanistan, Paghman.

*Phragmatobia fuliginosa* subsp. *nawari* Ebert, 1973, *Reichenbachia* 14 (8): 55-56. Holotype: Zentral Afghanistan, Dasht-i-Nawar, 3000m.

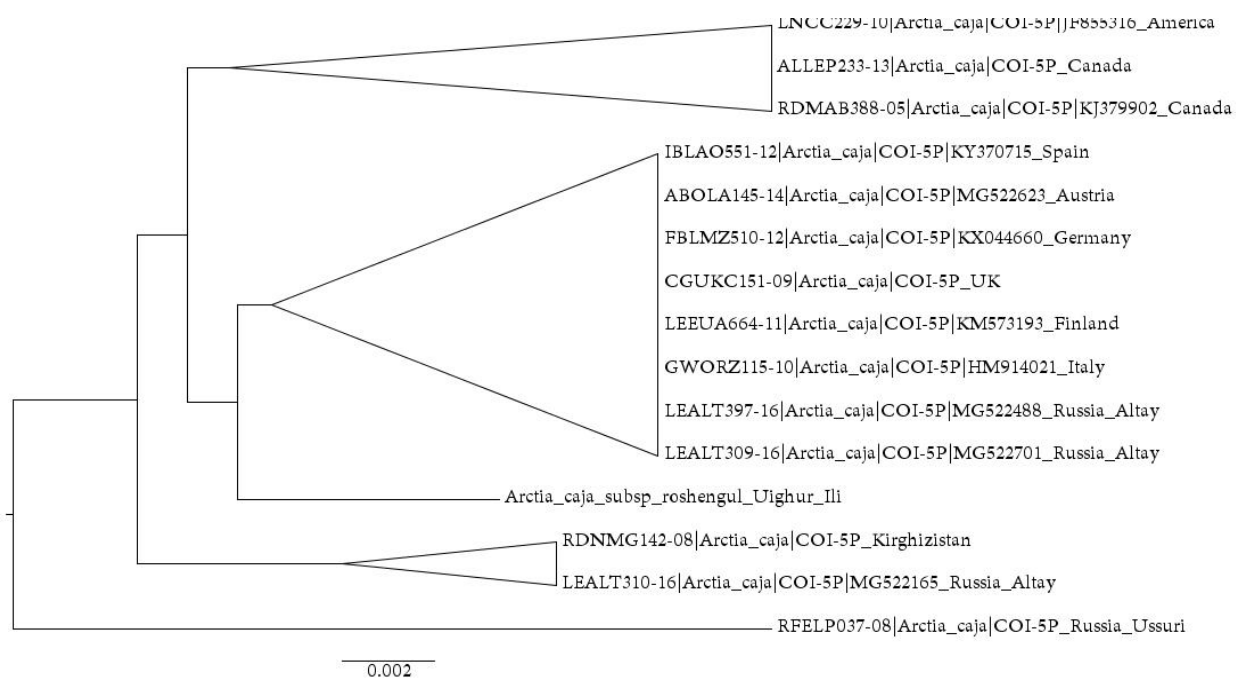
*Phragmatobia fuliginosa* subsp. *paghmani*: Dubatolov, 2010, *Neue ent. Nachr.* 65: 61 “Transcaucasia: Azerbaijan; Iran; northern Iraq; Afghanistan; Central Asia; southern Kazakhstan; China (western Xinjiang)” [Uighur Ili].

*Phragmatobia fuliginosa* subsp. *paghmani*: Kemal & Koçak, 2018, *Priamus* 17 (3): 212 “Ili Region, Tokuztara, Köndeleng”.

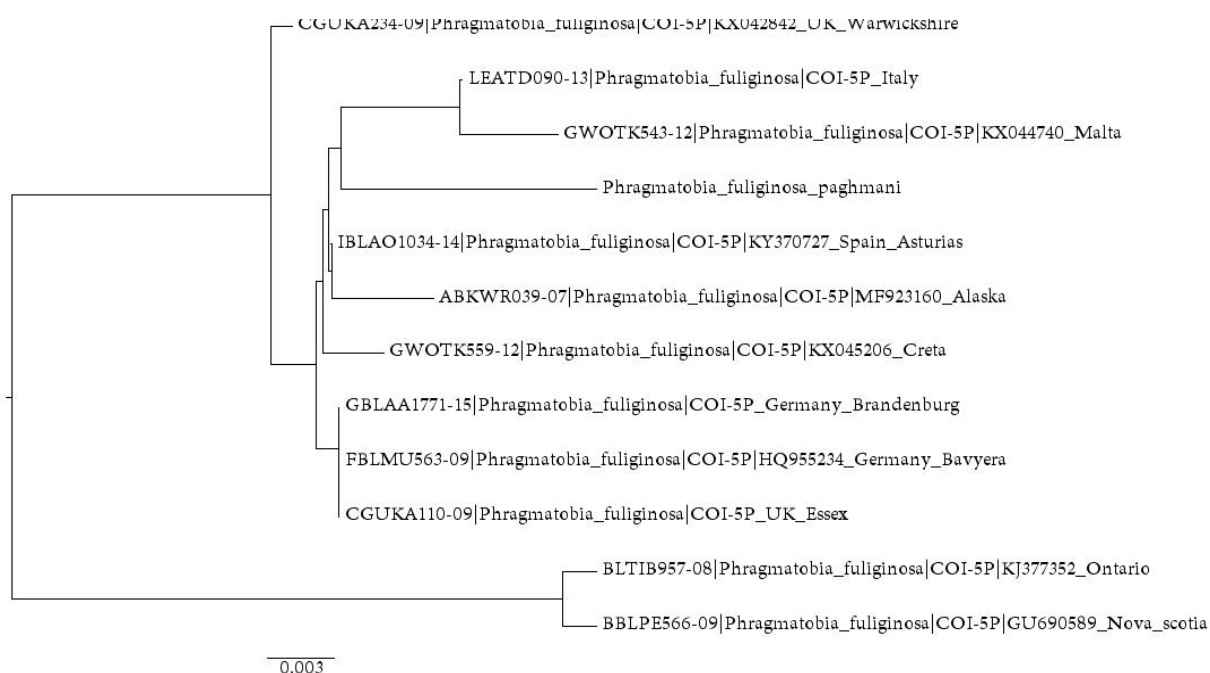
Range: Azerbaidjan, Iran, N. Iraq, Afghanistan, S. Kazakhstan, Uighur Ili, Köndeleng.

Comments: Dubatolov (2010) stated the distribution of this subspecies from northern Iraq to Central Asia. Therefore, the specimen captured from Köndeleng (Uighur Ili) considered by the authors as *paghmani* (Kemal & Koçak, 2018). In the present study, the first mtCOI gene sequence of *Phragmatobia fuliginosa paghmani* was obtained from population in Uighur Ili. In our phylogenetic tree, Uighur Ili population is located with the populations of Malta and Italy in same clade (respectively 0.020 and 0.019), but it is genetically closest to the Spanish population (0.012).

In the molecular phylogenetic analysis, *Phragmatobia fuliginosa paghmani* was separated from three phylogenetically distinct groups (Fig. 2). The first one is UK\_Warwickshire. The second one is Eurasian (other population of UK\_Essex). The third one is Canada. The pairwise Kimura's two-parameter distances among these three groups are large enough to judge that each group has been reproductively isolated for a long time. Dubatolov (2010) emphasized that the range of the subspecies *paghmani* from northern Iraq to Uighur. However, there is no molecular data reported from this region until now. Therefore, more data is needed from different geographies for the accurate phylogeny estimation of this subspecies.



**Fig. 1.** Neighbour-joining tree (Kimura 2-parameter) for *Arctia (s.str.) caja ssp. roshengul* based on 658bp of COI (barcode region).



**Fig. 2 -** Neighbour-joining tree (Kimura 2-parameter) for *Phragmatobia fuliginosa paghmani* based on 658 bp of COI (barcode region).

It is difficult to answer by systematics and evolutionary biologists to determine when and how geographic races differ from ancestral population and then to establish their present distribution. This study is rather narrative, although it is based on insufficient geographical data and our objective molecular phylogeny. However, we believe that this study is the most reasonable and initial at present. To make the phylogeny estimation of this groups more confirmatory, molecular phylogenetic analyses using more barcoding are require from different regions.



**Figs. 3, 4** - *Arctia caja* ssp. *roshengul* (holotype, ♀), at rest in nature, correct date on 10.viii.2005, from Tekes, Kichikkuşay (left); *Phragmatobia fuliginosa* ssp. *paghmani*, upperside of male, from Tokuztara (Köndeleng) (right), M. Kemal (Cesa)

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